

AMENDMENTS TO THE CLAIMS

This listing of the claims below replaces all prior versions and listing of claims in this application.

Claims 1-35: Cancelled

Claim 36. (Currently amended) A method for obtaining high vigor in a ~~plant~~ cell of an oilseed rape plant, an *Arabidopsis* plant or a corn plant, when compared to a control plant cell, comprising introducing a chimeric gene in said cell to yield a transgenic cell, wherein said chimeric gene comprises the following operably linked DNA regions:

- a) a plant-expressible promoter;
- b) a DNA region, which when transcribed yields a RNA molecule, ~~said RNA molecule being~~ capable of reducing the expression of endogenous PARP genes; and
- c) a DNA region involved in transcription termination and polyadenylation

wherein said RNA molecule for introduction into said cell of said oilseed rape plant or said *Arabidopsis* plant comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5, or and the nucleotide sequence of SEQ ID No: 10; and~~

- ii) an antisense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from the complement of ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5 or the nucleotide sequence of SEQ ID No: 10;~~

said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; or

wherein said RNA molecule for introduction into said cell of said corn plant comprises

- iii) a sense nucleotide sequence comprising a nucleotide sequence of 100 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, or SEQ ID No: 10; and

iv) an antisense nucleotide sequence comprising a nucleotide sequence of 100 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, or SEQ ID No: 10;
said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region;
and
wherein said vigor of said ~~plant~~ cell of an oilseed rape plant, an *Arabidopsis* plant or a corn plant can be measured by measuring the capacity of explants of said plant to reduce 2,3,5-triphenyltetrazoliumchloride.

Claim 37. (Currently amended) The method of claim 36, wherein said cell is a cell of a corn plant and wherein said sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 10 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 10.

Claim 38. (Currently amended) The method of claim 36, wherein said cell is a cell of an oilseed rape plant or a cell of an *Arabidopsis* plant and wherein said sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 5 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 5.

Claim 39. (Currently amended) The method of claim 36, wherein said cell is a cell of a corn plant and wherein said sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 3 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 3.

Claim 40. (Previously presented) The method of claim 36, wherein said plant expressible promoter is a constitutive promoter.

Claim 41. (Previously presented) The method of claim 36, further comprising the step of regenerating a transgenic plant from said transgenic plant cell.

Claim 42. (Previously presented) The method of claim 41, further comprising the step of producing more plants comprising said chimeric gene by a conventional breeding scheme.

Claim 43. (Cancelled)

Claim 44. (Currently amended) A transgenic oilseed rape, corn or *Arabidopsis* plant exhibiting high vigor when compared to a control plant, said transgenic oilseed rape, corn or *Arabidopsis* plant comprising in its cells a chimeric gene, ~~said chimeric gene comprises~~ comprising the following operably linked DNA regions:

- a) a plant-expressible promoter;
- b) a DNA region, which when transcribed yields a RNA molecule, ~~said RNA molecule being~~ capable of reducing the expression of endogenous PARP genes; and
- c) a DNA region involved in transcription termination and polyadenylation;

wherein said RNA molecule transcribed from said chimeric gene in said corn plant comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5 or the nucleotide sequence of SEQ ID No: 10; and~~
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from the complement of ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5, or the nucleotide sequence of SEQ ID No: 10;~~

said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; or

wherein said RNA molecule transcribed from said chimeric gene in said oilseed rape plant or *Arabidopsis* plant comprises

- iii) a sense nucleotide sequence comprising a nucleotide sequence of 100 consecutive nucleotides from SEQ ID No: 5; and
- iv) an antisense nucleotide sequence comprising a nucleotide sequence of 100 consecutive nucleotides from the complement of SEQ ID No: 5;
said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region
and
wherein said vigor of said plant can be measured by measuring the capacity of explants of said plant to reduce 2,3,5-triphenyltetrazoliumchloride.

Claim 46. (Currently amended) The transgenic plant of claim 45, wherein said plant is a corn plant and wherein sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 10 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 10.

Claim 47. (Currently amended) The transgenic plant of claim 45, wherein said plant is an oilseed rape plant or an Arabidopsis plant and wherein said sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 5 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 5.

Claim 48. (Currently amended) The transgenic plant of claim 45, wherein said plant is a corn plant and wherein said sense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the nucleotide sequence of~~ SEQ ID No 5 3 and said antisense nucleotide sequence comprises a nucleotide sequence of ~~about~~ 100 nucleotides ~~selected from the complement of the nucleotide sequence of~~ SEQ ID No 5 3.

Claim 49. (Currently amended) The ~~method~~ transgenic plant of claim 44 ~~[[47]]~~, wherein said plant expressible promoter is a constitutive promoter.

Claim 50. (Cancelled)

Claim 51. (Currently amended) A seed of the plant of claim 44 [[47]], comprising said chimeric gene.

Claim 52. (Currently amended) A chimeric gene ~~comprises~~ comprising the following operably linked DNA regions:

- a) a plant-expressible promoter;
- b) a DNA region, which when transcribed yields a RNA molecule, ~~said RNA molecule~~ being capable of reducing the expression of endogenous PARP genes; and
- c) a DNA region involved in transcription termination and polyadenylation;

wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5, or the nucleotide sequence of SEQ ID No: 10; and~~
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of ~~about~~ 100 consecutive nucleotides from the complement of ~~a nucleotide sequence selected from the group consisting of the nucleotide sequence of SEQ ID No: 1, the nucleotide sequence of SEQ ID No: 3, the nucleotide sequence of SEQ ID No: 5, or the nucleotide sequence of SEQ ID No: 10;~~
said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region.

Claim 53. (Previously presented) The chimeric gene of claim 52, wherein said plant expressible promoter is a constitutive promoter.

Claim 54. (New) The chimeric gene of claim 52, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180, and said nucleotide sequence of 100

consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the complement of the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the complement of the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180.

Claim 55. (New) The chimeric gene of claim 52, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705, and said nucleotide sequence of 100 consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the complement of the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the complement of the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705.

Claim 56. (New) The chimeric gene of claim 52, wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10.

Claim 57. (New) The chimeric gene of claim 52, wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10.

Claim 58. (New) The method of claim 36, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180, and said nucleotide sequence of 100 consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the complement of the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the complement of the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180.

Claim 59. (New) The method of claim 36, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705, and said nucleotide sequence of 100 consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the complement of the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the complement of the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705.

Claim 60. (New) The method of claim 36, wherein said RNA molecule comprises

- iii) a sense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- iv) an antisense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10.

Claim 61. (New) The method of claim 36, wherein said RNA molecule comprises

- iii) a sense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- iv) an antisense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10.

Claim 62. (New) The transgenic plant of claim 44, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180, and said nucleotide sequence of 100 consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No 1 from nucleotide position 113 to 1189, the complement of the sequence of SEQ ID NO 3 from nucleotide position 107 to 583, the complement of the sequence of SEQ ID No: 5 from nucleotide position 131 to 542, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 81 to 1180.

Claim 63. (New) The transgenic plant of claim 44, wherein said nucleotide sequence of 100 consecutive nucleotides from said sense nucleotide sequence is the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705, and said nucleotide sequence of 100 consecutive nucleotides from said antisense nucleotide sequence is the complement of the sequence of SEQ ID No: 1 from nucleotide position 2558 to 2704, the complement of the sequence of SEQ ID No: 3 from nucleotide position 1595 to 1747, the complement of the sequence of SEQ ID No: 5 from nucleotide position 1575 to 1724, or the complement of the sequence of SEQ ID No: 10 from nucleotide position 2559 to 2705.

Claim 64. (New) The transgenic plant of claim 44, wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of 250 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5 or SEQ ID No: 10.

Claim 65. (New) The transgenic plant of claim 44, wherein said RNA molecule comprises

- i) a sense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10; and
- ii) an antisense nucleotide sequence comprising a nucleotide sequence of 500 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, SEQ ID No: 5, or SEQ ID No: 10.

Claim 66. (New) A transgenic oilseed rape, corn or *Arabidopsis* plant exhibiting high vigor when compared to a control plant, said transgenic oilseed rape, corn or *Arabidopsis* plant comprising in its cells a chimeric gene comprising the following operably linked DNA regions:

- a) a plant-expressible promoter;
 - b) a DNA region, which when transcribed yields a RNA molecule capable of reducing the expression of endogenous PARP genes; and
 - c) a DNA region involved in transcription termination and polyadenylation;
- wherein said RNA molecule transcribed from said chimeric gene in said corn plant comprises
- i) a sense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from SEQ ID No: 1, SEQ ID No: 3, or SEQ ID No: 10; and
 - ii) an antisense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from the complement of SEQ ID No: 1, SEQ ID No: 3, or SEQ ID No: 10;
- said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region; or

wherein said RNA molecule transcribed from said chimeric gene in said oilseed rape plant or *Arabidopsis* plant comprises

- iv) a sense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from SEQ ID No: 5; and
 - v) an antisense nucleotide sequence comprising a nucleotide sequence of about 100 consecutive nucleotides from the complement of SEQ ID No: 5;
- said sense nucleotide sequence and said antisense nucleotide sequence being capable of combining into a double stranded RNA region
and

wherein said vigor of said plant can be measured by measuring the capacity of explants of said plant to reduce 2,3,5-triphenyltetrazoliumchloride.